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Searched:

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Minimum DB seq length: 0
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centromere protein E - human N; Alternate names: centromere C: Species: Homo sapiens (man) C; Date: 03-Mar-1994 #sequence_ C; Accession: $28261
                                                                                              RESULT
S28261
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C;Accession: F85016
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488
A;Accession: F85016
A;Status: preliminary
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C;Genetics:
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-
C;Accession: F85016
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                   #sequence_revision 03-Mar-1994 #text_change 19-Jan-2001
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21.5%;
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C;Genetics:
A;Gene: SPDB:SPAC1F3.06c
                                                           A; Residues: 1-1957 <CON>
A; Cross-references: EMBL
                                                                                                        A;Status: preliminary; translated A;Molecule type: DNA
                                                                                                                                                                                          R; Connor, R.; Churcher, C.M.; submitted to the EMBL Data Lil
                                                                                                                                                                                                                                                           hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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C;Superfamily: centromere protein E; kinesin motor domain homology
C;Keywords: ATP; coiled coil; microtubule binding; mitosis; nucleotide
E;7-335/Domain: kinesin motor domain homology <KMOT>
F;86-93/Region: nucleotide-binding motif A (P-loop)
E;486-2183/Domain: coiled coil #status predicted <COI>
E;486-2183/Domain: coiled coil #status predicted <COI>
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A:Title: CENP-E is a putative kinetochore mot A; Reference number: S28261; MUID:93024922

A; Accession: S28261

A; Molecule type: mRNA
A; Residues: 1-2663 <YEN>
A; Cross: references: EMBL: Z15005; NID:929864;
                                            A;Cross-references: EMBL:Z70690; PID A;Experimental source: strain 972h-;
                                                                                                                                                  A; Accession: T38077
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A;Cross-references: GDB:361164; OMIM:117143
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Best Local Similarity
Matches 93; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSEKTDKLSNMQKDLENSNAKLQEKIQELKANEHQLITLKKDVNETQKKVSEMEQLKKQI 1856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNATVVSLQQALGKAEMLCSTLKKQMKYLEQQQDET----KQAQEEAG----RLRSKMKT 165
                                                                                                                                                                                                                                                                                                                                                                                                                    IQELQKKELQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDKLRGIVSEKTNEISNMQKDLEHSNDALKAQDLKIQEELRIAHMHLKEQQETIDKLRGI 1796
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                                                                                                                                                                                                                   Barrell,
                                            PIDN:CAA94624.1;
2h-; cosmid c1F3
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Pred. No. 0.048;
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                                                                                                                                                                                            ll, B.G.; Rajandream,
April 1996
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                                                                GSPDB:GN00066;
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                                                                  SPDB:SPAC1F3.06c
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chromosomal protein XCAP-C - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 02-Jun-2000
C;Accession: A55094
R;Hirano, T; Mitchison, T.J.
Cell 79, 449-458, 1994
A;Title: A heterodimeric coiled-coil protein required for mitotic chromosome A;Reference number: A55094; MUID:95042742
A;Accession: A55094
A;Status: preliminary
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A55094
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C; Keywords:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-1290 <HIR>
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Best Local Similarity
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                                                                                                                                                                                                                                                   ---NKL------FDLAQEEENVLDREF------LKNELDNVRAQLSQKDKEKRDS
                                                                                                                                                                                                                                                                                              DEKYDVAISSSCGALDHI--VVDTIDTA----QECVNFLKKQNVGVATFIGLDKMKVWE
                                                                                                                                                                                                                                                                                                                              DHSRDVA-AIHCGHTFHLQCLIQSFETAPSRTCPQC----RIQVGKRTII-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDNQLATNKLKNQLDHLNQEIRLKEDVLKEKESLIISLEESLSNQRQKESSLLDAKNELE 1445
   DQ----
                                NQQKQMEKNLETLKKEYEKVAEKAGKVEAEVKRLHKLIVDINNHKLKAQQDKLDKVTKEI
                                                                SAVEQLAVYCVSLKKEYENLKE-ARKASGEV-----ADKLRKDLFSSRSKLQTVYSEL
                                                                                                 QDRKAHLEEEVAKLRQATREMKNTFEKYTASLQSLSEQEVHLKAQVKELEVNVAAAAAPDK
                                                                                                                               QDETKQAQEEAGRLR-----SKMKTMEQIELLLQSQLPEVEEMIRDMGVGQ 191
                                                                                                                                                                ---VVTLQGQIIEQSGTMTGGGGKVMKGRMGSSVMVEISDDQLQKMENKLKTDTTRATEI
                                                                                                                                                                                             QVIIDTLRDTLEERNATVVSLQQALGKAEMLCSTLKK----QMKYLEQQ-------
                                                                                                                                                                                                                             KGLNKIQTPENIPRLFDMVKVKDEQIKPAFYFALRDTIVANNLDQATRVAFQKDKRWR--
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                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosomal protein; DNA condensation;
                                                                                                                                                                                                                                                                                                                                                               Conservative
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   -AKLELKSAQKDLQSA----
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22.1%;
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                                                                                                                                                                                                                                                                                                                                                                            Score 182.5; DE Pred. No. 0.037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 183.5; DB Pred. No. 0.054;
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 -DKEIMSLKKKLTMLQETL----
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                                                                            hypothetical protein T07C4.10a - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text C:Accession: T24635; S41023 R:Buck, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: 1427.
R;Henkhaus, J.; Wohldmann, P.
submitted to the EMBL Data Library,
submitted for the sequence of C. el
submitted to the EMBL Data A; Reference number: Z19915 A; Accession: T24635 A; Status: preliminary; trar A; Molecule type: DNA
                                                                                                                                                                RESULT
T24635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 2
A;Introns: 64/3; 99/3; 165/1; 267/3; 350/2;
C;Superfamily: RING finger homology
F;188-238/Domain: RING finger homology <RRN>
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A; Residues: 1-425
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A; Accession: T25457
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23.0%;
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               from
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Pred. No. 0.
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                                                               February 1995
                                                                                                                15-Oct-1999 #text_change
                 GB/EMBL/DDBJ
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hypothetical protein B0432.9 - Caenorhabditis elegans C; Species: Caenorhabditis elegans
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A;Experimental source: strain Bristol N2; clone B0432
                                                                                                                                                                                                                                                   117 TVVSLQQAL----GKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 IRALCTICSDFFDHSRDVAAIHCGHTFHLQCLIQSFETAPSRTCPQCRIQVGKRTIINKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NECKEAECSLPEV-QEQHRSLLQEIKAIQEKEHALQKEAL--NIRLNIE-QIDSHIAE-H 1022
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                                                                                                                                                                                                                                                                                                                                                                                                                         LQGSCSICFEDLKQNDKISAIVCGHIYHHGCISQWIAT--KRQCPSCRRTVPKNGFVEKL
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                                               DLFSSRSKLQTVYSELDQAKLELKSAQKDLQSADKEIMSLKK 269
                                                                                                                                                     LQSQLPEVEEMIRDMGVGQSAVEQLAVYC ----VSLKKEYENLKEARKASGEVADKLRK
                                                                                                                                                                                                          TVKSLEKKIIREKDKYRQEIPKLQATINHLTISSEETAYLKRELQESKNRLKTCEFYKIL
-AAKEIEQLKMEVQS----LKRAAQEDAAIKK 424
                                                                                                   -SSEADKQLGEYLKKNGNLDTEKFFQLMKSTNK----DLTDKRRE
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Legans cosmid
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01-Dec-2000

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myosin heavy chain - chicken (fragment)
c;Species: Gallus gallus (chicken)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997
C;Accession: I51302
                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNAA;Residues: 1-764 <YUT>
                                                                                                                                                                              Development 120, 871-883, 1994
A;Title: Expression of the atrial-specific myosin A;Reference number: I51302; MUID:95324374
A;Accession: I51302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-1138 <WIL>
A;Cross-references: EMBL:Z48055; PIDN:CAAB8136.1; GSPDB:GN00021; CESP:T07C4.10a
A;Experimental source: clone T07A5
R;BerKs, M.
submitted to the EMBL Data Library, January 1994
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                                                                                                      A;Cross-references: GB:S78540; C;Superfamily: myosin heavy cha
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A; Residues: 895-1138 <BER>
A; Cross-references: EMBL: 229443
C; Genetics:
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A;Introns: 16/1; 124/3; 146/3; 204/1; 311/3; 358/3; 615/3; 900/2; 961/3; 1008/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: S41014
A; Accession: S41023
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Best Local :
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 RIQVGKRTIINKLFFDLA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLRKEHEGQMAELEKRLEKVSEKEKEAIEQLEKIQKENKTIVKENVY-LSESKQVLLESE
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                               Conservative
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                                                                                                                                                                                                                             J.T.; Bader, D.
883, 1994
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22.48;
                                            7.5%;
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                                                                                                         chain;
                                                                                                      NID:g1000404; PIDN:AAB34772.1; PID:g1000405 ain; myosin motor domain homology
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                               68;
                       Score 178.5; DB 2;
Pred. No. 0.032;
"" smatches 127;
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Pred. No. 0.049
-QEEENVLDR----EFLK-NELDNVRAQLSQKDKEKRD
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A;Accession: JE0343
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-477 <CGA>
C;Superfamily: rfp transforming protein; RING finger homology
F;12-71/Domain: RING finger homology <RRN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Jul-1999 #sequence_revision 16
C;Accession: JE0343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Ogawa, S.; Goto, W.; Orimo, A.; Hosoi, T.; Ouchi, Y.; Muramatsu, M.; Inoue, S. Biochem. Biophys. Res. Commun. 251, 515-519, 1998
A;Title: Molecular cloning of a novel RING finger-B box-coiled coil (RBCC) protein, A;Reference number: JE0343; MUID:99011410
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C;Species: Ra
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Best Local
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                                           282 PVASETVDRLVLESPAPVEVNLKLRRPSFRDDI 314
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                                                                                                                                                                                                                  MEQIELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKL
  PVAIKTVCRV---
                                                                                    GK-LQDSKASLDHQSRSLDLTLLQLEEQTQQEPLQMLQDVKDTLTRKESLSMQYPEVVL-
                                                                                                                                                                                                                                                                  REAQEHRMHRVLPLDEAAREYKL----RLEEDIKYLREEMMKTETLQAKEEQTLTEWQERV 178
                                                                                                                                                                                                                                                                                           RDTLEERNATVVSLQQALGKAEMLCSTLKKQMKYL--EQQQDETKQAQEEAGRLRSKMKT
                                                                                                                                                                                                                                                                                                                                                                                                KRTI-INKLF---FDLAQEEENVLDREFLKNELDNVRAQLSQKDKE---KRDSQVIIDTL
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                                                                                                                             RKDLFSSRSKLQTVYSELDQAKLEL--KSAQKDLQSAD--KEIMSLKKKLTMLQETLNLP
                                                                                                                                                                           KERRERILE----EFQKVVLFL-----VEEEPRLLQILKKEED--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QSADKEIMSLKKKLTMLQETL------NLPPVASETVDRLVLESPAPVEVNLKLRRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KHRLQNEVEDLMADVERSNAAAAALDKKQRNFDKILSEWK---QKFEESQTELEASQKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQVIIDTLRDTLEE----RNATVVSLQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381
-PGQIEV-LK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 178; DB : Pred. No. 0.019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-Jul-1999 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- ALEEAEASLEHEEGKILKAQLEFNQVKAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114;
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                                                                                      273
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revisior
C;Accession: T22976; T23157
R;Lightning, J
submitted to the EMBL Data Library, J
A;Reference number: Z19645
A;Accession: T22976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Nolecule type: DNA
A; Residues: 1-1133 <WI2>
A; Cross-references: EMBL. 266514; PIDN: CAA91344.1;
A; Cross-references: clone KO1A11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: clone C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, A; Reference number: Z19700 A; Accession: T23157
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A;Cross-references: EMBL:Z34801; PIDN:CAA84332.1; GSPDB:GN00021; CESP:F59A2.6
A;Experimental source: clone F59A2
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A; Introns: 13/2; 43/3; 107/3; 413/3; 492/3; 567/3;
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밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Species: Caenorhabditis elegans
;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
;Accession: T22976; T23157
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Best Local
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492
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EINVLTT-SLAEKEQQT
                                                                                                                                                                     KSHSPIQ------DVPK--KICKGPRKESQLSL-GGQSCAGEPDEELVGAFPIFVRNAI
                                                                                                                                                                                                                                                                                                                                                                                                                    VSKKLDSSETSLKEFSDMIEAMKIQLINCEKQKDEAVELLKQ-KLEEVEKNMSDVEVQKQ
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                               RVRVKTVPSLFQAKLDT
                                                                                                 LGQKQPKRPRSESSCSKDVVRT---GFDGLGGRTKFIQPTDTVMIRPLPVKPKTK--VKQ 448
                                                                                                                                    EKHTGIQRAQGALDDAEKEVKVLKEQLERAQSALESSQELASSQKADKIQELEKELQNA-
                                                                                                                                                                                                                                         ASETVDRLVLESPAPVEVNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLE
                                                                                                                                                                                                                                                                            SSAISEITKQMEAAKKELEASEKEKSELREQMDRLQKVHNAGQEDIQKLQKTWELEMAKI
                                                                                                                                                                                                                                                                                                               -SELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQET----
                                                                                                                                                                                                                                                                                                                                                 LLLESTTSEMKQHAEAAEIVKKQ---LEEAQSS----IENLKKDAENERN-LKTALESDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEQQQDETKQAQEEAGRLRSKMKTM------EQIELLLQSQLPEVEEMIRDMGVGQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSQKDKEKRDS-QVIIDTLRDTLEERNATVVS-----LQQALGKAEMLCSTLKKQMKY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDALQAEVNEAKALREEIQAKYDDVTQKAERIQGELEESKKVLESEKQAFENEKEQEREE
                                                                  ----QKRSSEELETANEMVRSLTATLENSNSETEILKQKLETLDKELQARQQTEKALTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.4%;
Similarity 20.5%;
                                                                                                                                                                                                                                                                                                                                                                      -SAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQTVY----
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                                 465
                                                                                                                                                                                                          -KLAREQLAGELE-NAKEDL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 177.5; DE Pred. No. 0.059;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSPDB:GN00021; CESP:F59A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         635/3;
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                                                                                                                                                                                                                                                                                                               -LNLPPV
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                                                                                                                                                                                                          KVVEE
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A;Molecule type: DNA
A;Residues: 1-1156 <AQF>
A;Cross-references: GB:AE000699; NID:g2983238;
A;Experimental source: strain VF5
C;GenetLos:
A;Gene: xcpC
C;Superfamily: chromosome segregation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome assembly protein homolog - i
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
B70356
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A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing A;Reference number: A69250; MUID:98049343
A;Recession: E69444
A;Accession: E69444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome segregation protein (smc1) homolog - Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Jun C;Accession: E69444
                                                                                                                                                                                                                                                                                       A;Title: The complete genome of the hyperthermophilic A;Reference number: A70300; MUID:98196666 A;Accession: B70356
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A;Residues: 1-1156 <KLE>
A;Cross-references: GB:AE000995; GB:AE000782;
C;Superfamily: chromosome segregation protein
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E69444
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R;Deckert, G.; Warre
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                                                                                                                                                                                                                                                      A; Status: preliminary; nucleic acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                353-358,
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21.4%;
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; Pred. No. 0.068;
89; Mismatches 116;
                                                                                                                                                 NID: g2983238;
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SMC1
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                                                                                                                                                    PIDN: AAC06839.1;
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C;Superfamily: myosin heavy chain; myosin motor domain homology C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylat F;92-775/Domain: myosin motor domain homology <MMOT> F;182-189/Region: nucleotide-binding motif A (P-loop) F;184-576/Region: actin binding #status predicted F;660-682/Region: actin binding #status predicted F;660-682/Region: actin binding #status predicted COI> F;128-1247/Domain: coiled coil #status predicted <COI> F;1228-1247/Domain: coiled coil #status predicted <COI> F;1248-1482/Domain: coiled coil #status predicted <CO2> F;1248-1482/Domain: carboxyl-terminal <CBT> F;133/Modified site: NG,NG,NG-trinethyllysine (Lys) #status predicted F;188/Binding site: ATP (Lys) #status predicted
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A27224
A27224
myosin heavy chain II - Acanthamoeba castellanii
N;Contains: myosin ATPase (EC 3.5.1.32)
C;Species: Acanthamoeba castellanii
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change C;Accession: A27224
C;Accession: A27224
R;Hammer III, J.A.; Bowers, B.; Paterson, B.M.; Korn, E.D.
J. Cell Biol. 105, 913-925, 1987
A;Title: Complete nucleotide sequence and deduced polypeptide servicesion: A27224
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                                                                                                                    Similarity 23.4
97; Conservative
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                                                                                                                7.4%; Score 176; DB 1; Length 1509; 23.4%; Pred. No. 0.099; tive 74; Mismatches 156; Indels 8
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                                                                                                AESRAEASDLQDKV-----KEITDTLHAELQAERSSSSALHTKLSKFSDEIATGHKELT
                                                                                                                                    MSLKKKLTMLQETLNLPPVASETVDRLVLESPAPVEVN--LKLRRPSFRDDI-----DLN
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C;Accession: T13030
R;Lantz, V.A.; Miller, K.G.
J. Cell Biol. 140, 897-910, 1998
                                                                                                                                                                                                                        microtubule binding protein D-CLIP-190 - fruit fly C;Species: Drosophila melanogaster C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999
                              A; Title: A class VI unconventional myosin A; Reference number: Z17588; MUID:98139549 A; Accession: T13030
A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -TGGASSEEVKRLEGE--LERLEEELLTA------
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A; Nolecule type: mRNA A; Molecule type: mRNA A; Residues: 1-1690 <LAN> A; Cross references: EMBL:AF041382; NID:g2773362; PID:g2773363; PIDN:AAB96783.1 A; Cross references: Extain Oregon R A;Cross-references: FlyBase:FBgn0020503 C;Keywords: cytoskeleton 835 QVQLEQLQQQAAASGEEGSKTVAKLHDEISQLKSQAEETQSELKSTESNLEAKSKQLEAA 210 --NLKEARKASGEVAD---KLRKDLFSSRSKLQTVYSELDQAKLELKSAQKDLQSADKEI 108 RDTLEERNATVVSLQQALGKAEMLCSTLKKQMK-YLEQQQDETKQAQEEAGRLRSKMKTM 166 724 QIQLEKESIEQQL--ALKQNELEDFQKKQSESEVHLQEIKAQNTQKDLELVESGESLKKL 50 RIQVGKRTIINKLFFDLAQEEENVLDREFLKNE--LDNVRAQLSQKDKEKRDSQVIIDTL 107 Local Similarity les 84; Conserv E-QIELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYE-----QQQLEEKTLGHEKLQAAL-----EELKKEKETIIKEKEQELQQLQSKSAESESALKVV Conservative 7.3%; 84; Mismatches 157; Pred. Score 175; DB : Pred. No. 0.13; 2; Length 1690; Indels Gaps 264 894 781 209 13;

-DTPPARPSSSQHGYYEKLCLEKSHSPIQDVPKKIC 357

317

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myosin heavy chain [similarity] - slime mold (Dictyostelium discoideum) N;Contains: myosin Arpase (EC 3.6.1.32) C;Species: Dictyostelium discoideum C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 02-Feb-: C;Accession: A26655, A24728; S00250 R;Marrick, H.M.; De Lozanne, A.; Leinwand, L.A.; Spudich, J.A. Proc. Natl. Acad. Sci. U.S.A. 83, 9433-9437, 1986 A;Hitle: Conserved protein domains in a myosin heavy chain gene from Dic A;Reference number: A26655; MUID:87092266 A;McCession: A26655
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C.Date: 09-Jun-2000 #sequence_revision 09-Jun-2000
C.Accession: A59293
R;Maeda, K.; Hostinova, E.; Roesc.Kleinkauf, A.; Sc submitted to GenBank, July 1995
A;Description: Isolation, sequencing of myosin heav A;Reference number: A59293
A;Accession: A59293
A;Accession: A59293
A;Accession: A59293
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A.Cross references: GB:032574; NID:9940232; PIDN:AAA74199.1; PII A.Experimental source: strain New Zealand White; cell type skeld: c; Genetics: A.Genetics: A.Gene: MHC C; Superfamily: myosin heavy chain; myosin motor domain homology F:89-769/Domain: myosin motor domain homology <MMO>
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Pred. No. 0.22;
2; Mismatches 148
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R; Wagle, G.; Noegel, A.; Scheel, J.; Gerisch, G.
FEBS Lett. 227, 71-75, 1988
A; Title: Phosphorylation of threonine residues on cloned fragments of the A; Reference number: $00250; MUID:88112226
A; Reference number: $00250
A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
A; Residues: 1734-1893 <WAG>
C; Comment: The rod domain is highly periodic, containing a pattern of 7
C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Keywords: actin binding; ATP; coiled coil; hydrolase; nucleotide bind F; 1-818/Domain: myosin motor domain homology <MMOT>
F; 819-2116/Domain: myosin motor domain homology <MMOT>
F; 819-2116/Domain: alpha-helical rod <ROD>
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                                     A; Molecule type: mRNA
A; Residues: 1-1999 < SUN>
A; Cross-references: EMBL: X62659
A; Cun, W.; Chantler, P.D.
Biocham. Biophys. Res. Commun.
                                                                                                                                                                                                                                                             J. Mol. Biol. 224, 1185-1193, 1992
J. Mol. Biol. 224, 1185-1193, 1992
A;Title: Cloning of the CDNA encoding a national control of the CDNA encodes in the CDNA encodes
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S21801
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C; Accession: S21801; pN0013; S18134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       myosin heavy chain, neuronal [similarity] -
N;Alternate names: myosin II
N;Contains: myosin ATPase (EC 3.6.1.32)
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A; Residues: 2035-2116 <DEL>
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LESPAPVEVNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLEKSHSPIQDV 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LALENLQNQKRSVE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKKICKGPRKESQLSLGGQSCAGEPDEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVRLQ---SELDDLTVRLDSETKDKSELLRQKKKLEEELKQVQEAL----AAETAAKLA 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSKLQTVYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQETLNLPPVASETVDRLV 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEEELEEMKR-VNDGQSDTISRLEKIKDELQKEVEELTES--FSEESKDKGVLEK----T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
Res. Commun. 175, 244-249, 199 cellular myosin II exhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESQL----VAVNNELDEE 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.28;
27.48;
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differential expression

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A;Reference number: PN0013; MUID:91151356
A;Accession: PN0013
A;Accession: PN0013
A;Accession: PN0013
A;Accession: PN0013
A;Residues: 1914-1998,'I' <SU2>
A;Experimental source: brain
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding: ATP; coiled coil; hydrolase; methylated amino a
F;84-763/Domain: myosin motor domain homology <MMOT>
F;84-763/Domain: myosin motor domain homology <MMOT>
F;174-181/Region: nucleotide-binding motif A (P-loop)
F;41-575/Region: actin binding #status predicted
F;836-1275/Region: actin binding #status predicted
F;836-1276/Region: coiled coil #status predicted
F;836-1276/Region: 1ight meromyosin
F;1277-1999/Region: light meromyosin
F;127/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
F;937,03/Active site: Cys #status predicted
F;1916/Binding site: phosphate (Ser) (covalent) #status predicted
F;1943/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                        RESULT 18
S54871
M protein -
                                                                                                                              M protein - Streptococcus sp.
C; Species: Streptococcus sp.
C; Date: 08-Jul-195 #sequence_revision 21-Jul
C; Accession: $54871
R; Podbielski, A.; Melzer, B.
submitted to the EMBL Data Library, June 1991
A; Reference number: $54871
A; Accession: $54871
A;Molecule type: DNA A;Residues: 1-532 <POD>
A;Residues: 1-532 <POD>
A;Cross references: EMBL:X60097; NID:g840905; PIDN:CAA42693.1; PID:g840906 C;Superfamily: M5 protein
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                                                                                                          A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 DKEKRDSQVIIDTLRDTLEERNATVVSLQQALGKAEMLCSTLKKQM------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 QCRIQVGKRTIINKLFFDLAQEEENVLDREF------LKNELDNVRAQLSQK 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -PKRPRSESSCSKDVVRTGFDGL 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKKMEDSVGCLETAEEVKRKLQKDLEGLS----QRHEEKVAAYDKLEKTKTRLQQELDDLL 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKKI-----CKGPRKESQLSLGGQSCAGEPDEELVGAFPIFVRNAILGQKQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEMIRDMGV-----GQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKOKRDIGEELEALKTELEDITDSTAAQQELRSKREQEVNIIKKTLEEEAKTHEAQIQEM 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELKMQLAKKE--EELQAALARVEEEAAQKNMALKKIRELESQISELQEDLESERASRNKA 1129
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18.7%; Pred. No. 0.24;
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                                                                                                                                                                                                                                                     21-Jul-1995 #text_change 26-Aug-1999
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 Ma Qu	Ouery Match 7.1%; Score 170; DB 2; Length 532; Best Local Similarity 21.5%; Pred. No. 0.059; Matches 82; Conservative 67; Mismatches 141; Indels 92; Gaps 12;
Qy	AQEEENVLDREFLK
Db	159 KMKVVNDSYQNTKREYDLIEEELGKKLKENQDLEEKLKDKEFYLGETLRYINELDLKLGQ 218
Qy	KDKEKRDSQVIIDTLRDTLEERNATVVSLQQ
 Db	219 LNIDNIDLKHELEQEKQKAEADRQT-LEAEKAKLEEEKQISDASRQSLRRDLDASREAKK 277
Qy	138 QMKYLEQQQDETKQAQEEAGR-LRSKMKTMEQIELLLQSQLPEVEEMIR 185
Db	778 QLEAEYQKLEEEKQISDASRQSLRRDLDASREAKKQLEAEYQKLEEQNKISEASRKGLRR 337
Qy	IGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFS
Db	338 DLDASREAKKOVEKDLANLTAELDKVKEEKQISDASRKGLRRDLDASRE 386
Qy	LNLPPVASETVDRLVLESPAPVEVNL
Db	387 AKKQVEKALEEANSKLAALEKLNKELEESKKLTEKEKAELQAKLEA 432
Qy	306 RRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLEKSHSPIQDVPKK 355
Дb	433 EAKALKEKLAKQAEELAKLRAGKASDSQTPEATPGNKVVPGKGQAPQAGTKPN 485
ОУ	356 ICKGPRKESQLSLGGOSCAGEP 377
Db	486 QNKEPMKETKROLPSTGEATNP 507
 RESULT A70387	
C; Sp	8-May-199
R; De	cession: A/U38/ ckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
Nature A;Titl	Nature 392, 353-358, 1998 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666
A; Ac	A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Mo	A;Molecule type: DNA A;Residues: 1-978 <aqf> A:Gross-references: GR:AEG00718: NTD:G2983504: DTDN:AAC07092 1: DTD:G2983515: GB:AEG0</aqf>
A; Ex C; Ge	ce: strain VF5
A;Ge C;Su	;Gene: aq_1006 ;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032
Qu Ma	Query Match 7.1%; Score 170; DB 2; Length 978; Best Local Similarity 22.6%; Pred. No. 0.12; Matches 79; Conservative 70; Mismatches 125; Indels 76; Gaps 13;
Qy	41 APSRTCPQCRIQVGKRTIINKLFFDLAQEEENVLDREFLKNE 82
Db	481 SPGDTCPVCGGIYRGKALENVDAEGISELKHAKELKEKEEREIDTTLKLYAQKINSLKEE 540
Qy	83 LDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQQALGKAEMLCSTLKKQMKYL 142
Db	ERIKKL
Qy	43 EQQQDETKQAQEEAGRLRSKMKTMEQIELLLQSQL-PEVEEMIRDMGVGQSAVEQLAVYC 20
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R; Hemmati-Brivanlou, A.; Mann, R.W.; Harland, R.M.
Neuron 9, 417-428, 1992
A;Title: A protein expressed in the growth cones of
A;Reference number: JH0720; MUID:92398961
A;Accession: JH0720
A;Molecule type: mRNA
A;Residues: 1-1744 <HEMS
A;Cross-references: GB:M99387; NID:g214816; PIDN:AA
A;Experimental source: tadpole head
C;Keywords: intermediate filament
                                                                                                                                                                                                                                                  myosin heavy chain, skeletal muscle, embryonic - rat N;Contains: myosin ATPase (EG 3.6.1.32)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001 C;Accession: A24922; A2538; B24263
R;Strehler, E.E.; Strehler-Page, M.A.; Perriard, J.C.; Periasamy, M.; Nadal J. Mol. Biol. 190, 291-317, 1986
A;Title: Complete nucleotide and encoded amino acid sequence of a mammalian
                     A; Molecule type: DNA
A; Residues: 1-1940 <STR>
A; Residues: 1-1940 <STR>
A; Cross references: GB:X04267; GB:X05004; NID:g56658; PIDN:CAA27817.1;
A; Cross references: GB:X04267; GB:X05004; NID:g56658; PIDN:CAA27817.1;
A; Strebler, E.E.; Mahdavi, V.; Periasamy, M.; Nadal-Ginard, B.
J. Biol. Chem. 260, 468-471, 1985
J. Biol. Chem. 260, 468-471, 1985
A; Title: Intron positions are conserved in the 5' end region of myosin
A; Reference number: A22538; MUID:85080119
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C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change
C;Accession: JH0720
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A; Accession: A24922
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A; Accession: A22538
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25.7%;
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Pred. No. 0.26;
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A: Variety: group G C;Date: 07-Sep-1994 #sequence\_revision 03-N C;Accession: S45599; S43554 R;ben Nasr, A.; Wistedt, A.; Ringdahl, U.; Eur. J. Biochem. 222, 267-276, 1994 A;Title: Streptokinase activates plasminoge

A; Status: preliminary A; Accession: S45599

A; Reference number: S45598; MUID: 94291620

plasminogen-binding protein MLG72 C; Species: Streptococcus sn.

Streptococcus

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03-Nov-1995 #text\_change

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A;Introns: 68/3; 116/3; 169/1
A;Note: the list of intron positions may be incomplete C;Superfamily: myosin heavy chain; myosin motor domain to C;Reywords: actin binding; ATP; coiled coil; hydrolase; F;89-767/Domain: myosin motor domain homology <MMOT>F;179-186/Region: nucleotide-binding motif A (P-loop) F;549-586/Region: actin binding #status predicted F;656-678/Region: actin binding #status predicted F;840-1940/Domain: coiled coil #status predicted F;840-180/Region: S
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A;Residues: 1358-1490,'G' <PER>
A;Cross-references: GB:K03468; NID:9205573; PIDN:AAA41652.1; PID:9205574
A;Experimental source: clone pMHC-72
C;Genetics:
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F;130/Modified site: N6,N6,N6-trimethyllysine (Lys)
F;185/Binding site: ATP (Lys) #status predicted
F;696,706/Active site: Cys #status predicted
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A; Cross-references: GB:
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1415 LEKT 1418
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                                                                                                                               SGEVADKLRKDLFSSRSKLQT----VYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTM
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23.0%;
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Pred. No. 0.3;
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R; Mahdavi, V.; Lompre, A.M.; Chambers, A.P.;
Eur. Heart J. 5, 181-191, 1984
A; Title: Cardiac myosin heavy chain isozymic
A; Reference number: 153305; MUID:85179510
A; Accession: 167441
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1871-1935 KRES
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         R;Mahdavi, V.; Periasamy, M.; Nadal-Ginard, B.
Nature 297, 659-664, 1982
                                                                                                                                                                                                                                                         A; Accession: S07536
A; Status: nucleic acid sequence not shown A; Molecule type: mRNA
A; Residues: 1-950, 'RK', '953-1935 <MCN>
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A; Molecule type: mRNA
A; Residues: 1-1935 < KRA>
A; Cross references: EMBL:X15939; NID:956656; PIDN:CAA34065.1; PID:956657
A; Cross references: EMBL:X15939; NID:956656; PIDN:CAA34065.1; PID:956657
A; MCNally, E.M.; Kraft, R.; Bravo-Zehnder, M.; Taylor, D.A.; Leinwand, L
J. Mol. Biol. 210, 665-671, 1989
A; Title: Full-length rat alpha and beta cardiac myosin heavy chain sequel
A; Reference number: S07535; MUID:90133919
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  A; Title: Molecular characterization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASREAKKQVEKALEEANSKLAALEKLNKELEES-----KKLTEKEKAELQAKLE
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Pred. No. 0.058;
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65 DLAQEEENVLDREFLKN---ELDNVRAQLSQKDKEKR------DSQVIIDTLRDTLEER 114

ELESSQLKIADLEHLKTLQPELETLQKHVGQKEEEEVSYLVGQLGEKEQTLTTVQTEMEEQ 1369

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A; Accession: A02989
A; Accession: A02989
A; Accession: A02989
A; Cross: I524-1528, 'V',1530,'R',1532-1730,'H',1732-1783,'K',1785-1850,'N',1852-185
A; Cross: references: GB:J00752; NID:g205577; PIDN:AAA41654.1; PID:g205578
C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Keywords: actin binding; ATP; Cardiac muscle; coiled coil; heart; hydrolase; methyl
F; 88-766/Domain: myosin motor domain homology <MVOT>
F; 178-185/Region: nucleotide-binding motif A (P-loop)
F; 548-585/Region: actin binding #status predicted
F; 839-1935/Domain: coiled coil #status predicted
F; 839-1935/Domain: coiled coil #status predicted
F; 839-1297/Region: Signature of the company of the collection of the collectio
                                                                                                                                                                                       A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: I-3187 <TOK> A;Residues: I-3187 <TOK> A;Residues: I-3187 <TOK> A;Cross references: DDBJ:D25543; NID:g516825; PIDN:BAA05026.1; PID:g516826 A;Crosment: This protein plays a role in the formation and maintenance of the characte C;Superfamily: giantin F;49-549,624-1176,1238-1707,1763-3114/Domain: coiled-coil leucine zipper #status pred F;3165-3187/Domain: membrane anchor #status predicted <MAD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Accession: JC5837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Toki, C.; Fujiwara, T.; Sohda, M.; Hong, H.S.; Misumi, Cell Struct. Funct. 22, 565-577, 1997
A;Title: Identification and characterization of rat 364-k
A;Reference number: JC5837; MUID:98093490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364K Golgi complex-associated protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 20-Jun-2000
C;Accession: JC5837
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F:129/Modified site: N6.N6.V6-trimethyllysine (Lys)
F:184/Binding site: ATP (Lys) #status predicted
F:695,705/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: nucleic acid sequence not shown
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                                        Query Match
Best Local (
    Matches
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                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSKLQT - - - - VYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQET
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    89; Conser
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                                7.1%;
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                                    Score 168.5; D
Pred. No. 0.61;
    Mismatches
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.32;
                                                                         DB 2;
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    160;
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    Indels
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    127;
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transcytosis-associated protein p115 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 23-Mar:1995 #sequence_revision 05-Apr:1995 #te)
C;Accession: A55913
R;Barroso, M.; Nelson, D.S.; Sztul, E.
Proc. Natl. Acad. Sci. U.S.A. 92, 527-531, 1995
A;Title: Transcytosis-associated protein (TAP)/p115 is
A;Reference number: A55913; MUID:95132633
A;Accession: A55913
A;Status: preliminary
A;Mc1catins: preliminary
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A; Residues: 1-959 <BAR>
A; Cross-references: GB: C; Keywords: membrane fu
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Best Local S
Matches 76
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                                                                                                                                                                                                       SSEEDKKEEEV-----KKTLEQHDNIVTHYKNVIREQDLQLEELKQQVSTLKCQNEQLQT
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ASGEVADKLRKDLFSSRSKLQTVYSELDQAKLELKSAQKD------LQSADKEIMSLKK
                                                                                              QVLLQSQLAEKDTVIENLRSSQVSGMSEQALATCSPRDAEQVAELKQELSALKSQLCSQS
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                                                                                                                         ELLLQSQLPEVEEMIRDM------GVGQSAV------EQLAVY-----
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Pred. No. 0.15
56; Mismatches
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A; Introns: 15/3;
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hypothetical protein T10G3.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #to C;Accession: T24806 R;Burton, J. submitted to the EMBL Data Library, October 1996 A;Referrence number: Z19937 A;Accession: T24806
                                   A; Molecule type: mRNA
A; Residues: 1-1325 <KON>
A; Cross-references: EMBL:D78270; NID:d1096175;
A; Experimental source: strain CD-1
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-1164 <WIL>
A;Description: supposed to play some role C;Keywords: leucine zipper
                                                                                                                                                          A; Title: Cloning and molecular characterization A; Reference number: Z22242; MUID:97217683 A; Accession: T42722
                                                                                                                                                                                                                     C; Accession: T42722
R; Kondo, M.; Sutou, S.
DNA Seq. 7, 71-82, 1997
                                                                                                                                                                                                                                                                              male-enhanced antigen-2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision
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                                                                                                                                          A;Status: preliminary; translated
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62; Conserv
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                  for spermatogenesis
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hypothetical protein KIAA0477 - human
C;Species: Homo sapiens (man)
C;Species: O1-Feb-1999 #sequence_revision O1-Feb-1999 #text_change 21-Ju1-2000
C;Accession: T00259
R;Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
DNA Res. 4, 345-349, 1997
A;Title: Characterization of cDNA clones in size-fractionated cDNA libraries from human A;Reference number: Z14085; MUID:98116662
A;Accession: T00259
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1132 <SEK>
A;Cross-references: EMBL:AB007946; NID:93413915; PIDN:BAA32322.1; PID:g3413916
C;Genetics: A;Note: K1AA0477
C;Keywords: alternative splicing
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Best Local S
Matches 77
                                                                                                                                                                                                                                                                                                Query Match 7.0%;
Best Local Similarity 22.8%;
Matches 91; Conservative 8
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                                                                                                131
                                                                                                                                       654
                                                                                                                                                                                                                 601 HLNHSLSHKEQLLQEF-----RELLQYRDNSDKTLEANEML--LEKLRQRIHDKAVALER
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                                                                                                                                                                                                                                                         24 HCGHTF-HLQCLIQSFETAPSRTCPQCRIQVGKRTIINKLFFDLAQEEENVLDREF-LKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity nes 77; Conserv
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                                                                                  LCSTLKKQMKYLEQQQDETK----QAQEEAGRLRSKMKTMEQIELLLQSQLPEVEE----
                                                                                                                                                        ELDNVRAQLSQKDKEKRDSQVII------DTLRDTLEERNATVVSLQQALG----KAEM 130
                  MIRDMGVGQSAV-EQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSK---
                                                       L-STTCQNLQWLKEEM-ETKFSRWQKEQES-----IIQQLQTSLHDRNKEVEDLSAT
                                                                                                                                     AIDEKFSALEEKEKELRQLRLAVRERDHDLERLRDVLSSNEATMQSMESLLRAKGLEVEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLKEARKASGEVADKLRKDLFSSRSKLQTVYSELDQAKLELKSAQKDLQSADKEIMSLKK
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                                                                                                                                                                                                                                                                                              b; Score 167.5;b; Pred. No. 0.2;82; Mismatches
<del>-</del>::
                                                                                                                                                                                                                                                                                                                                     DB 2;
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A; Introns: 6/2;
A; Note: F5E19_70
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A; Residues: 1-853 <SAT>
A; Cross-references: EMBL:AL391147
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A; Accession: T51505
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                                       EVIF
                                                                            RTGF
                                                                                                                                                                                                                                  VNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLEKS-----HSPIQDVP 353
                                                                                                                                                                                                                                                                                                                                                       YVKKMEEDVA-SMGKEMNRLDNLLKRTEEEADAAWKKEAQTKDSLKEVEEEIVYLQETLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---MEQIELLLQSQLPEVEEMI----RDMGVGQSAVEQLAVYCVSLKKEYENLKEA----
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                                                                                                                                                      KKICKGPRKESQLSLGGQSCAGEPDEELVGAFPIFVRNAILGQKQPKRPRSESSCSKDVV
                                                                                                                                                                                               ENGELSES--EKDYDL-----LPKVVEFSSENGH--RSVEEKSAKVETLDHEPPQE--
                                                                                                                                                                                                                                                                           EAKAESMKLKENLLDKETEFQNVIHENEDLKAKEDVSLKKIEELSKLLEEAILAKKQPEE
                                                                                                                                                                                                                                                                                                                SADKEIMSLKKKL------TMLQETLNLPPV--ASETVDRLVLESPAPVE 300
                                                                                                                                                                                                                                                                                                                                                                                              -- RKASGEVADKLRKDLFSSRSKLQTVYSELD-----QAKLELKSA-----QKDLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                   ETQIDDLKLVIKATNEKYENMLDEARHEIDVLVSAVEQTKKHFESSKKDWE~MKEANLVN 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KSHSPIQDVPKKICKGPRKESQLSLGG-QSCAGEPDEEL
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Similarity 21.9%; Pred. No. 0.15;
93; Conservative 80; Mismatches 141;
                                       767
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79/3
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Sequence Database,
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August 2000
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110;

Gaps

19;

495

214

165

613 258

673

763

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A;Title: Molecular cloning and pre-mRNA maturation of Onchocerca A;Reference number: A48575; MUID:93165084
A;Recession: A48575
A;Status: preliminary; not compared with conceptual translation A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-879 CDAH>
A;Note: sequence extracted from NCBI backbone (NCBIP:125109) C;Superfamily: myosin heavy chain; myosin motor domain homology
                                                           R;Collier, V.L.; Kronert, W.A.; O'Donnell, Genes Dev. 4, 885-895, 1990
A;Title: Alternative myosin hinge regions :
A;Reference number: A35815; MUID:90346288
A;Accession: A35815
                                                                                                                                                              myosin heavy chain 1, muscle - fruit fly (Drosophila melanogaster) (fragment) (Species: Drosophila melanogaster C;Date: 12-oct-1990 #sequence_revision 28-Mar-1991 #text_change 20-Jun-2000 C;Accession: A35815
                                                                                                                                                                                                                                          RESULT
A35815
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c;Species: Onchocerca volvulus
c;Species: Onchocerca volvulus
C;Date: 01-Dec:1993 #sequence_revision 18-Nov-1994 #text_change 05-Jun-1998
C;Accession: A48575
C;Accession: A48575
C;Accession: A6; Gallin, M.; Schumacher, M.; Erttmann, K.D.
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A; Residues:
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                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                        В
;Molecule type: DNA :Residues: 1-1201 <COL>
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Best Local Similarity 19.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VNLKLRRPSFRDDI-DLNATED-----VDTPPARPSSSQHGYYEKLCLEKSHSPIQDVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DQAKLELKSAQKDLQSADKEIMSLKKKLTMLQETLNLPPVASETVDRL---VLESPAPVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QDDLHEAKEALADANRKLHELDLENARLAGEIRELQTALKESEAARRDAENRAQRALAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YENLKEARKASGEVADKLRK-DLFSSR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEQLEKTVMELKVRIDELTVELEAAQREARAALAELQKMKNLYEKAVEQKEALARENKKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEDLRKKMLQKQAEYEEQIEIMLQKISQLEKAKSRLQSEVEVLIVDLEKAQNTIAILERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --EMLCSTLKKQMKYLEQQQ---DETKQAQEEAGRLRSKMKTM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSQLQAQLHQVQLELDSVRTALDEESAARAEAEHKLALANTEITQWKSKFDAEVALHHEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DSQVIIDTLRDTLEERNATVVSLQQALGKA------
                                                                                                                                                                                                                                                                                                                        ----GRI----TDLVSIN----NNLTAIKN--KLETELSTAQADLD
                                                                                                                                                                                                                                                                                                                                                             RTGFDGLGGRTKFIQPTDTVMIRPLPVKPKTKVKQRVRVKTVPSLFQAKLD
                                                                                                                                                                                                                                                                                                                                                                                                      DQYALAQRKVSALSAELEEC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                       KKICKGPRKESQLSLGGQSCAGEPDEELVGAFPIFVRNAILGQKQPKRPRSESSCSKDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEIARLKKKYQAEIAELEMTVDNLNRANIEAQKTIKKQSEQLKVLQASLEDTQRQLQQTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQLRIEM---ERRLQEKEEEMEALRKNMQF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -EQIELLLQSQLPEVEEMIRDMGVGQ-------SAVEQLAVYCVSLKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 167; DB 2; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  ----KVALDNAIRARKQAEIDLEEAN---
                                                                                                      are
                                                                                                                                           P.T.;
                                                                                                      utilized
                                                                                                                                         Edwards,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----EIDRLTAALADAEARMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160;
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                                                                                                                                         K.A.; Bernstein,
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                                                                                                    tissue-specific
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                                                                                                                                         S.I.
                                                                                                      fashion
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A;Cross-references: E
A;Note: the authors t
C;Genetics:
A;Gene: FlyBase:Mhc
A;Cross-references: E
C;Superfamily: myosir
C;Keywords: ATP
                                                                RESULT
B35815
myosin heavy chain 2, muscle - fruit fly (Drosophila melanogaster) (fragment) (?Species: Drosophila melanogaster C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 20-Jun-2000 C;Accession: B35815
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Best Local Similarity
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Keywords: ATP
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                                                                                                                                    1167
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                                                                                   32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAEALRMKKKLEADINELEIALDHANKANAEAQKNIKRYQQQLKDIQTALEEEQRARDDA 905
                                                                                                                                                                  LGQKQPKRPRSESSCSKDVVRTGFDGLGGRTKF
                                                                                                                                                                                                                                   KKICKGPR-----
                                                                                                                                                                                                                                                                                                     VEVNL-----KLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLEKSHSPIQDVP
                                                                                                                                                                                                                                                                                                                                       AQTQEKLRKALEQQIKELQVRLDEAEANALKGGKKAIQKLEQRVRELENELDGEQRRHAD
                                                                                                                                                                                                                                                                                                                                                                      LQSADKEIMSLKKKLTMLQETLNLPPV-----ASETVDRLVLE------SPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                        SGEVADKLRKDLFSSRSKLQTVYSELDQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTMEQIEL-----LLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEQEENKVLRAQL---ELSQVRQEIDRRIQEKEEEFENTRKNHQRALDSMQASLEAEAKG 845
                                                                                                                                   VGRGASPAPRATS----
                                                                                                                                                                                                   DKLQQKIKTYKRQIEEAEEIAALNLAKFRKAQQELEEAEERADLAEQAISKFRAKGRAGS
                                                                                                                                                                                                                                                                      AQKNLRKSERRVKELSFQSEED----
                                                                                                                                                                                                                                                                                                                                                                                                         NASISAAKRK-----LESELQTLHSDLDELLNEAKNSEEKAKKAMVDAARLADELRAEQDH 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R--EQLGISERRANALQNELEESRTLLEQADRGRRQAEQ-----ELADAHEQLNEVSAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -ERNATYVSLQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase:FBgn0002741 in heavy chain; myos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL:x53155; NID:g8219; PIDN:CAA37310.1; PID:g2546938 translated the codon TGC for residue 649 as Lys, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.0%;
                                                                                                                                                                                                                                   -----KESQLSLGGQSCAGEPDEELVGAFPIFVRNAI 393
                                                                                                                                    -VRPQFDGLAFPPRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 167; DB
Pred. No. 0.23
76; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 myosin
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. 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Genes Dev. 4, 885-895, 1990
A;Title: Alternative myosin hinge regions are utila;Réference number: A35815; MUID:90346288
A;Status: Profission: B35815 A;Gene: FlyBase:Mhc
A;Cross-references: FlyBase:FBgn0002741
C;Superfamily: myosin heavy chain; myos A;Molecule type: DNA
A;Residues: 1-1201 <COL>
A;Cross-references: EMBL:X53155; NID:g8219; PIDN:CAA37311.1;
A;Note: the authors translated the codon TGC for residue 649 Query Match
Best Local Similarity
Matches 93; Conserv :Keywords: Genetics: 7.0%; 20.5%; Score 167; Pred. No. 0 myosin motor DB 2; .23; utilized domain Edwards, K.A.; Length 1201; in a tissue-specific fashion PID:g2546939 as Lys, and Lys, Bernstein, AAG S.I. for

resi

d

Conservative

76;

Mismatches

144;

Indels

140;

Gaps

15;

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A:Cross-references: FlyBase:FBgn0002741
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Superfamily: nucleotide binding; P-loop
F:137-1032/Domain: myosin motor domain homology #status atypical <MMO>
F:227-234/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R/George, E.L.; Ober, M.B.; Emerson Jr., C.P. Mol. Cell. Biol. 9, 2957-2974, 1989
A;Title: Functional domains of the Drosophila A;Reference number: A32491; MUID:89384556
A;Accession: B32491
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 33
B32491
B32491
myosin heavy chain 2, muscle - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Species: 12-Cct-1999 #sequence_revision 31-Dec-1993 #text_change 02
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                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M61229; A;Note: the authors translated
                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA; mRNA
A; Residues: 1-2411 <GEO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: B32491
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Best Local
 2116
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                               164 KTMEQIEL-----LLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257
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                                                                                                                                                                                                                Local
                                                                                                                                                                66 LAQEEENVLDREFLKNELDNVRAQLSQKDKEK-----RDSQVIIDTLRDTLE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66
                                                                                                                             LEQEENKVLRAQL---ELSQVRQEIDRRIQEKEEEFENTRKNHQRALDSMQASLEAEAKG
                                                               KAEALRMKKKLEADINELEIALDHANKANAEAQKNIKRYQQQLKDIQTALEEEQRARDDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGRGASPAPRATS-----VRPQFDGLAFPPRF 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGQKQPKRPRSESSCSKDVVRTGFDGLGGRTKF 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKLQQKIKTYKRQIEEAEEIAALNLAKFRKAQQELEEAEERADLAEQAISKFRAKGRAGS 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQKNLRKSERRVKELSFQSEED - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEVNL-----KLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLEKSHSPIQDVP 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQTQEKLRKALEQQIKELQVRLDEAEANALKGGKKAIQKLEQRVRELENELDGEQRRHAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NASISAAKRK----LESELQTLHSDLDELLNEAKNSEEKAKKAMVDAARLADELRAEQDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGEVADKLRKDLFSSRSKLQTVYSELDQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R--EQLGISERRANALQNELEESRTLLEQADRGRRQAEQ-----ELADAHEQLNEVSAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KTMEQIEL------LLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAEALRMKKKLEADINELEIALDHANKANAEAQKNIKRYQQQLKDIQTALEEEQRARDDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAQEEENVLDREFLKNELDNVRAQLSQKDKEK-----RDSQVIIDTLRDTLE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQSADKEIMSLKKKLTMLQETLNLPPV-----ASETVDRLVLE------SPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----ERNATVVSLQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEQEENKVLRAQL---ELSQVRQEIDRRIQEKEEEFENTRKNHQRALDSMQASLEAEAKG
                                                                                                                                                                                                                     Similarity
EQLGISERRANALQNELEESRTLLEQADRGRRQAEQ-----ELADAHEQLNEVSAQ
                                                                                                                                                                                                       Conservative
                                                                                           -- ERNATVVSLQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKM
                                                                                                                                                                                                                     7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----KESQLSLGGQSCAGEPDEELVGAFPIFVRNAI
                                                                                                                                                                                                                                                                                                                                                                                                           GB:M27194
the codon
                                                                                                                                                                                                     76;
                                                                                                                                                                                                                   Score 167; DB 2;
Pred. No. 0.52;
                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             TGC
                                                                                                                                                                                                                                                                                                                                                                                                             for residue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               melanogaster muscle
                                                                                                                                                                                                     144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #text_change 02-Feb-2001
                                                                                                                                                                                                                                     Length 2411;
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                                                                                                                                                                                                     Indels 140;
                                                                                                                                                                                                                                                                                                                                                                                                             329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myosin heavy-chain
                                                                                                                                                                                                   Gaps
2167
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                                 217
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                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                      150
                                                                                                                                                                                123 QALGKAEMLCSTLKKOMKYL----EQQQ------DETKQAQEEAGRLRSKMKTMEQIEL 171
                                                                                                                                                                                                                                                     77
                                                                                                                                                                                                                                                                                                                      22 AIHCGHTFHLQCLIQSFETAPSRTCPQCRIQVGKRTIINKLF---FDLAQEEENVLDR--
                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 94; Conserv
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SNQKLRVTEQVLTEKEGELKRIEAKHLE----

EQALLEEKIATTHETYRGLIKEISERVD

SRSKLQTVYSELDQAKLELKSAQ-KDLQSADKEIMSLKKKLTMLQETL-NLPPVASETVD

KALLEQEAAYNTLSQEHKQINGLFEEREATIKKLTDDYKQAREMLEEYMSKMEETER---

LLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFS

231

321

374

RMQETGKDVASRESAIVDLEETVESLRNEVERKGDEIESLMEKMSNIEVKLRL

AVESEHQEILKKLKESDE-----ICGNLRVETEKLTSENKELNEKLEVAGETESDLNQKL

Conservative

75;

Pred. No. 0.09 5; Mismatches

173;

Indels

77;

Gaps

14;

76

204

EFLKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNA------TVVSLQ

EDVKKERDGLEAELASKAKDHESTLEEVNRLQGQKNETEAELEREKQEKPALLNQINDVQ

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C;Accession: C96667

C;Accession: C9667

C;Accession: C9667

C;Accession: C9667

C;Accession: C96667

C;Accession: C9667

C;A
                                                                                                                                                                                                                    A;Gene:
A;Map po
                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-555 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown pr
C; Species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 02-Mar-2001 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE005173; NID:g10645401; PIDN:AAG21519.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2224
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                                                                                                                                                                                                                          position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein, 71502-69704 [imported] - Arabidopsis thaliana
es: Arabidopsis thaliana (mouse-ear cress)
02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change
                                                                                                                                                                                                                                                                                F15H21.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKICKGPR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQTQEKLRKALEQQIKELQVRLDEAEANALKGGKKAIQKLEQRVRELENELDGEQRRHAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQSADKEIMSLKKKLTMLQETLNLPPV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NASISAAKRK----LESELQTLHSDLDELLNEAKNSEEKAKKAMVDAARLADELRAEQDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGEVADKLRKDLFSSRSKLQTVYSELDQ-------AKL--ELKSAQKD
7.0%;
22.4%;
Score 166.5; DB Pred. No. 0.095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KESQLSLGGQSCAGEPDEELVGAFPIFVRNAI
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                                                           DВ
                                                      2;
                                                           Length
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RESULT 35
A59234
Slow myosin heavy chain 3 - quail
C;Species: Coturnix coturnix
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 08-Sep-2000
C;Accession: A59234
R;Nikovits Jr., W; Wang, G.F.; Feldman, J.L.; Miller, J.B.; Wade, R.; Nelson, L.
J. Biol. Chem. 271, 17047-17056, 1996
A;Title: Isolation and characterization of an avian slow myosin heavy chain gene
A;Reference number: A59234; MUID:96291845
A;Accession: A59234
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1931 <NIK>
A;Cross-references: GB:U53862; NID:91289513; PIDN:AAC59912.1; PID:91289514
C;Superfamily: myosin heavy chain; myosin motor domain homology
F;81-761/Domain: myosin motor domain homology
RESULT 36
A49545
A49545
Plasminogen-binding protein PAM precursor - Streptocock
plasminogen-binding m-like protein
C; Species: Streptococcus pyogenes
C; Date: 23 Mar-1995 #sequence_revision 05-Apr-1995 #te:
C; Accession: A49545; S61084; S60829; S70459; S32619
R; Berge, A.; Sjoebring, U.
J. Biol. Chem. 268, 25417-25424, 1993
A; Title: PAM, a novel plasminogen-binding protein from A; Reference number: A49545; MUID:94064605
A; Accession: A49545
A; Molecule type: DNA
A; Residues: 1-388 <BER>
A; Cross-references: EMBL: Z22219; NID:9288978; PIDN:CAAPA; Cross-references: EMBL: Z22219; NID:9288978; PIDN: ZAAPA; Cross-
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPARPSSSQHGYYEKLCLEKSHSPIQDVPKKICKGPRKESQLSLGGQSCAGEPDEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERSNAAAAALDKKQRNFDKILSEWK---QKFEESQTELEASQKEARSLSTELFKLKNAYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEELEEAKKKLAQRLQEAEE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QDVPKKICKGPRKESQLSLGGQSCAGEPDEELVGAFPIFVRNAILGQKQPKRPRSESSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESLEHLETFKRENKNLQEEISDLTEQLGASQKSIHELE-KVRKQLDAEKLELQA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---MEQIELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKK-----EYENLK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -TMLQETLNLPPVASETVDRLVLESPAPVEVNLKLRRPSFRDDIDLNATFDVDT
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Pred. No. 0.43;
74; Mismatches
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8978; PIDN:CAA80222.1; Musser, J.; Kehoe, M.
                                                                                                                                                                                                                                                                                                                                                                          Streptococcus
ke protein (Pd
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                                                                                                                                                                                   Streptococcus
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53)
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                                   PID: g940870
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C;Keywords: cell wall
F;1-29/Domain: signal sequence (fragment) #ste
F;30-388/Product: plasminogen-binding protein
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A:Experimental source: serotype M53
R:Carlsson Wistedt, A.; Ringdahl, U.; Mueller-Esterl, W
M01. Microbiol. 18, 569-578, 1995
A;Title: Identification of a plasminogen-binding motif
A:Reference number: S70457; MUID:96342385
A:Accession: S70459
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A; Residues: 17-77 <WHW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Whatmore, A.M.; Kapur, V.; Mol. Microbiol. 14, 619-631,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U11975; NID:g533627; A;Experimental source: serotype M53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 13-96 <WHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, July 1994
A;Description: Noncongruent relationships between variation
A;Reference number: S61072
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A; Residues: 30-162 <CAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local :
                                                                 328
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381 L 381
                               368 L
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                                                                                                                                  EEANSKLAALEKLNKELEES
                                                                                                                                                                                                                                  RKDLFSSRSK-----LQTVYSELDQAKLE---
                                                                                                                                                                                                                                                                    EKQISDASRQGLR----RDLDASREAKKQVEKDLANLTAELDKVKEEKQISDASRQGL
                                                                                                                                                                                                                                                                                                   MEQIELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKL
                                                                                                                                                                                                                                                                                                                                       KLADKQEHLNGA---
                                                                                                                                                                                                                                                                                                                                                                                                        DLREKEEELQGLKDDVEKLTADAELQRLKNERHEEAELERLKSERHDHDKKEAERKALED
                                                                 AEELAKLRAEKASDSQTPDAKPGN--
                                                                                                A-----TFDVDTPPARPSSSQHGYYEKLCLEKSHSPIQDVPKKICKGPRKESQLS
                                                                                                                                                                 QSADKEIMSLKKKLTMLQETLNLPPVASETVDRLVLESPAPVEVNLKLRRPSFRDDIDLN
                                                                                                                                                                                                 RRDLDASREAKKQVEKGLANLTAELDKVKEEKQISDASRQGLRRDLDASREAKKQVEKAL
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73; Conserv
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631, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 166;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                     -----LRYINEKEAEAKEKEAE----QKKLKE
                                                                 KAVPGKGQAPQAGTKPNQNKAPMKETKRQ
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tein PAM
                                                                                                                                  KKLTEKEKAELQAKLEAEAKALKEQLAKQ
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M1 protein precursor - Streptococcus pyogenes C:Species: Streptococcus pyogenes C:Date: 19-Mar-1997 #sequence\_revision 19-Mar C:Accession: S46489; S46490 R:Akesson, P.; Schmidt, K.H.; Cooney, J.; Bjo Biochem. J. 300, 877-886, 1994

19-Mar-1997 #text\_change 07-May-1999

S46489 RESULT

37

Biochem. J. A; Title: M1

protein and

protein

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IgGFc-

and Bjoerck,

albumin-binding

streptococcal surface

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A;Reference number: $46489; MUI.
A;Accession: $46489
A;Molecule type: DNA
A;Residues: 1-484 <AKE>
A;Experimental source: strain 4-
A;Accession: $46490
A;Accession: $46490
A;Rolecule type: protein
A;Residues: 42-51 <AKW>
A;Experimental source: strain 4-
                                                                                                                                                                                                                                             RESULT 38
T14867
T14867
C:Species: Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C:Accession: T14867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Genetics:
A;Gene: emml
C;Superfamily: M5 protein
C;Keywords: transmembrane protein
C;Keywords: transmembrane protein
F;1-41/Domain: signal sequence #status predicted
F;42-484/Product: M1 protein #status experimental
F;459-477/Domain: transmembrane #status predicted
                                               A; Gene: ab
A; Introns:
                                                                          A;Cross-references:
C;Genetics:
                                                                                                                                 A;Accession: T14867
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                         A; Reference number: Z18248; MUID: 98365468 A; Accession: T14867
                                                                                                                                                                                                                  R;Rivero, F.J.; Kuspa, A.; Brokamp, R.; Matzner, M.; Noegel, J. Cell Biol. 142, 735-750, 1998
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   Query Match
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Best Local
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                                                              abpD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEKLNKELEESKKLTEKEKAELQAKLEAEAKALKEQLAKQAEELAKLRAGKASDSQTPDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPEV--EEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QA-SQDYNRANVLEKELETITREQEINRNLLGNAKLELDQLSSEKEQLTIEKAKLEEEKQ
                                                                                                         -1738 <RIV>
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Similarity 21.6%;
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                                                                                            EMBL: AF057019;
                                                                                                                                                                                                an actin-binding protein
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   .0%;
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Pred. No. 0.086;
   Score
                                                                                         NID: g3549260; PID: g3549261; PIDN: AAC34582
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A;Molecule type: mRNA
A;Residues: 1-1935 <KOl>
A;Cross-references: GB:U75316; NID:g1698894; PIDN:AAB37320.1; PID:g1698895
A;Cross-references: Strain domestica
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: cardiac muscle; heart
F;88-766/Domain: myosin motor domain homology <MMO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                myosin heavy chain beta chain, cardiac - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000
C;Accession: A59286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A59286
A; Accession: A59286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to GenBank,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; not compared with conceptual translation
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Best Local Similarity
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289
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                                                                  QTVYSELDQAKLELKSAQKDLQSADKEIMSLKKKL---
                                                                                                                                                                                                                                                                                                                                             LKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEE----RNATVVSLQQALGKAEMLCST 134
DRLVLESPAPVEVNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLEKSHSP
                                          KQKYEE----SQSELESSQKEARSLSTELFKLKNAYEESLEHLETSKRENKNLQEEISDLT
                                                                                                                                                                              MGVGQSAVEQLAVYCVSLKK-----EYENLK---EARKASGEVADKLRKDLFSSRSKL
                                                                                                                                                                                                                           YEEETETKAELQRVLSKANSEVAQWRTKYETDAIQRTEELEEAKKKLAQRLQDAEE----
                                                                                                                                                                                                                                                                      LKKQMKYLEQQQDETKQAQEEAGRLRSKMKT.....MEQIELLLQSQLPEVEEMIRD
                                                                                                                                                                                                                                                                                                                     LSRQLDEKEALISQLTRGKLTYTQQLEDLKRQLEEEVKAKNALAHALQSARHAADLLREQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRPRSES-----SCSKDVVRTGFDGLGGRTKF
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                                                                                                                                  ----AVEAVNAKCSSLEKTKHRLQNEIEDLMVDVERSNAAAAALDKKQRNFDKILAEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QRPNQIEIDRLVNEIVNRNQDLIRK-----NKTKF 1651
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81; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 166; DB Pred. No. 0.45;
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                                                                                     TMLQETLNLPPVASETV 288
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bullous pemphigoid antigen 1 precursor - human
N;Alternate names: 230k bullous pemphigoid autoantigen; BP230 antigen
C;Species: Homo sapiens (man)
C;Date: 17-Jul-1992 #sequence_revision 11-Jul-1997 #text_change 21-Jul-2000
C;Accession: I56317; A40937; A40882; A61393; A37342; S46669
R;Elgart, G.W.; Stanley, J.R.
J. Invest. Dermatol. 101, 244-246, 1993
A;Title: Cloning of the 5' mRNA for the 230-kD bullous pemphigoid antigen by A;Reference number: I56317; MUID:93346806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
A40937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: the sequence from Fig. 3 1 R; Owaribe, K.; Kartenbeck, J.; Stu Differentiation 45, 207-220, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M69225
R;Tanaka, T.; Parry, D.A.D.; Klaus-Kovtun, J. Biol. Chem. 266, 12555-1259, 1991
A;Title: Comparison of molecularly cloned by A;Reference number: A40882; MUID:91286285
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                                                                                                                                                                                                                                                                                                      R;Hopkinson, S.B.; Jones, J.C.R.
Biochem. J. 300, 851-857, 1994
A;Title: Identification of a second protein
A;Reference number: S46669; MUID:94280413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: The hemidesmosomal plaque. Characterization of a major constituent A;Reference number: A37342; MUID:91216368
A;Accession: A37342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M63618; NID:g179518; PIDN:AAA35606.1; R;Sawamura, D.; Li, K.H.; Nomura, K.; Sugita, Y.; Christiano, J. Invest. Dermatol. 96, 908-915, 1991
A;Title: Bullous pemphigoid antigen: cDNA cloning, cellular eA;Reference number: A61393; MUID:91258872
A;Accession: A61393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-850,'G',852-1643,'T',1645-2363,'T',2365-2494,'V',2496-2542,'K',2544-2649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Human bullous pemphigoid antigen (BPAG1). Amino acid sequences deduced from A;Reference number: A40937; MUID:92011493
A;Accession: A40937
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                                                      A; Map position: 6; A; Introns: 2016/3
                                                                                                          A;Gene: GDB:BPAG1
A;Cross-references:
                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1897-2081 <HOP>
                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1595-1942, 'R', 1944-2202 <OWA>
A; Cross-references: GB: X58677; NID: g36094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem.
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                                                                                                                                                                                   A; Cross-references:
                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                    A; Accession: S46669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1722-2649 <SAW2>
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A; Residues: 555-2649 <TAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: I56317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: not compared with conceptual translation
          :Keywords:
                                    Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1514
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       list of introns is basement membrane;
                                                                                   6p12-6p11
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17784-17790, 1991
                                                                                                          GDB:125207; OMIM:113810
                                                                                                                                                                                 EMBL: U04850;
not complete
extracellular matrix; glycoprotein; membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 is inconsistent with the nucleotide sequence Stumpp, S.; Magin, T.M.; Krieg, T.; Diaz, L.A.;
                                                                                                                                                                                 NID: g451556;
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                                                                                                                                                                                                                                                                                                                                                                                                            PIDN:CAA41528.1;
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1742 EESGKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1378 AEQDMRELTYELNALQLEKTSSEEKARLLKDKLDETNNTLRCLKLELERKDQAEKGYSQQ 1437
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                                                                                                                                                                                                                     --VNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLEKSHSPIQDVPKKICK 358
                                                                                                                                                                                                                                                                                                                    HAVAEKNIQHLNSQIHSFRDEKELERLQICQRKSDHLKEQFEK---SHEQLLQNIKAEKE
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                                                                                           SKDVVRTGFDGLGGRTKFIQPTDTVMIRPLPVKPKTKVKQRVRVKTVPS-----LFQ
                                                                                                                                                        GPRKESQLSLGGQSCAGE---PDEELVGAFP-----IFVRNAILGQKQPKRPRSESSC 408
                                                             SKEEKRRGEQKVQLQQAQVQELNNRL-----
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No. 0.
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